

C/Accession: A26719; D38268; PH0949; I53715
B/Yamanashi Y. Enkuchito C T. Camba Y. Gub...

Mol. Cell. Biol. 7, 237-243, 1987

A:Title: The yae-related cellular gene lyn encodes a possible tyrosine kinase similar to

A:Reference number: A26719; PMID:87172710; PMID:1561390

A:Accession: A26719

A:Molecule type: mRNA

A:Residues: 1-512 <YAM>

A:Cross-references: GB:M16038; NID:G187268; PIDN:AAA59540.1; PID:G307144

A:Partners: J.; Maekelae, T.P.; Allitalo, R.; Lehtvaetho, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Purative tyrosine kinases expressed in K-562 human leukemia cells.

A:Reference number: A38268; PMID:91062389; PMID:2247464

A:Accession: D38268

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 369-424 <PAR>

A:Cross-references: GB:M16038; NID:G187268; PIDN:AAA59540.1; PID:G307144

A:Partners: J.; Maekelae, T.P.; Allitalo, R.; Lehtvaetho, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: Expression of the B cell-associated tyrosine kinase gene lyn in primary neurobl

A:Reference number: A38268; PMID:91062389; PMID:2247464

A:Accession: PH0949; PMID:92376604; PMID:1510669

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 369-424 <BIB>

A:Cross-references: GB:M16038; NID:G187268; PIDN:AAA59540.1; PID:G307144

A:Partners: J.; Maekelae, T.P.; Allitalo, R.; Lehtvaetho, H.; Allitalo, K.

Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A:Title: The cdna encoding two forms of the lyn protein tyrosine kinase are expressed i

A:Reference number: 153715; PMID:94171041; PMID:8125304

A:Accession: 153715

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-24, 46-512 <RID>

A:Cross-references: GB:M79321; NID:G187270; PIDN:AAA50019.1; PID:G187271

A:Experimental source: spleen form B

A:Gene: GDB:LYN

A:Cross-references: GDB:120159; OMIM:165120

A:Map position: 8q13-qter

A:Function: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

A:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote

F:2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>

F:2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT

F:70-118/Domain: SH3 homology <SH3>

F:129-226/Domain: SH2 homology <SH2>

F:245-504/Domain: protein kinase homology <KIN>

F:253-261/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Binding site: palmitate (Cys) (covalent) #status predicted

F:275/Active site: Lys #status predicted

F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.7%; Score 374.5; DB 1; Length 512;

Best Local Similarity 40.3%; Pred. No. 4, 2e-23;

Matches 81; Conservative 36; Mismatches 75; Indels 9; Gaps 3;

6 SRRKSLPSPSSSVQGGPVTMEERSKATVALGSPAGAPAEISLRGEPPLTVSD 65

38 SNKQKQPVPE-SQLLPQORFQTKPPEQGDIVVALYPIGTHPDLSFKKGKMKVLEH 96

66 GDMWTVLSEVSGREYNIPSYHAKV-----SHQWLYEGLSREKAEELLILPQNGAPFLIR 121

97 GEMWAKSLITKKEGPIPSNVYAKVNTLETETEMFKDITRKDAERQLAPNGSAGAPFLIR 156

122 ESOTRRGSGVSLNLSRPASMDIRIRHICLDNGWLYISPLTPSPSLOALVHYSELAD 181

157 ESETLKGSFSLVDFPDVPHGDIKHYKIRSLDNGYIISPRITFPICSDIMKHOKQAD 216

182 DICCLKEPCVLRAGAPLPCK 202

217 GLCRREKACI-----SPKPK 233

RESULT 3

156160

protein-tyrosine kinase (EC 2.7.1.112) lyn, splice form A - rat

N:Contains: protein-tyrosine kinase lyn, splice form B

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: 156160; 167811; 167812

J:Minoguchi, K.; Nishikata, H.; Stragmanian, R.P.

J:Immunol. 150, 222, 1993

A:Title: Bacterially expressed rat p56lyn binds several proteins in rat basophilic leu

A:Reference number: 156160

A:Accession: 156160

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-512 <MIN>

A:Cross-references: GB:L14951; NID:G294582; PIDN:AAA41549.1; PID:G294583

A:Partners: J.; Maekelae, T.P.; Allitalo, R.; Lehtvaetho, H.; Allitalo, K.

Gene 138, 219-222, 1994

A:Title: The cdna encoding two forms of the lyn protein tyrosine kinase are expressed i

A:Reference number: 153715; PMID:94171041; PMID:8125304

A:Accession: 167812

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-24, 46-230, 'L', 232-307, 'A', 309-418, 'Y', 420-512 <RID2>

A:Cross-references: GB:L14823; NID:G294580; PIDN:AAA20945.1; PID:G294581

A:Note: in Genbank entry RATTYNTYR, release 116.0 PIDN:AAA20945.1, the source is de

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprote

F:2-512/Product: protein-tyrosine kinase lyn, splice form A #status predicted <MATA>

F:2-24, 46-512/Product: protein-tyrosine kinase lyn, splice form B #status predicted <MAT

F:70-118/Domain: SH3 homology <SH3>

F:129-226/Domain: SH2 homology <SH2>

F:245-504/Domain: protein kinase homology <KIN>

F:253-261/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Binding site: Lys #status predicted

F:397,508/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.5%; Score 371.5; DB 1; Length 512;

Best Local Similarity 40.8%; Pred. No. 7, 4e-23;

Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;

6 SRRKSLPSPSSSVQGGPVTMEERSKATVALGSPAGAPAEISLRGEPPLTVSD 65

38 SNKQKQPVPE-SQLLPQORFQTKPPEQGDIVVALYPIGTHPDLSFKKGKMKVLEH 96

66 GDMWTVLSEVSGREYNIPSYHAKV-----SHQWLYEGLSREKAEELLILPQNGAPFLIR 121

97 GEMWAKSLITKKEGPIPSNVYAKVNTLETETEMFKDITRKDAERQLAPNGSAGAPFLIR 156

122 ESOTRRGSGVSLNLSRPASMDIRIRHICLDNGWLYISPLTPSPSLOALVHYSELAD 181

157 ESETLKGSFSLVDFPDVPHGDIKHYKIRSLDNGYIISPRITFPICSDIMKHOKQAD 216

182 DICCLKEPCVLRAGAPLPCK 202

217 GLCRREKACI-----SPKPK 233

RESULT 4

A39719

protein-tyrosine kinase (EC 2.7.1.112) lyn, long splice form - mouse

N:Contains: protein-tyrosine kinase lyn, short splice form

C:Species: Mus musculus (house mouse)

C:Date: 18-Feb-2000 #sequence revision 18-Feb-2000 #text_change 03-Mar-2000

C:Accession: A39719; B39750; B39750

R.Stanley, E.; Ralph, S.; McEwen, S.; Boulet, I.; Holtzman, D.A.; Lock, P.; Dunn, A.R.
 Mol. Cell. Biol. 11, 3399-3406, 1991
 A>Title: Alternatively spliced murine lyn mRNAs encode distinct proteins.
 A.Reference number: A39719; MUID:9126068; PMID:1710766
 A.Accession: A39719
 A.Molecule type: mRNA
 A.Residues: 1-512 <STA>
 A.Cross-references: GB:M64608; NID:g198938; PIDN:AAA3470.1; PID:g198939
 A.Accession: B39719
 A.Molecule type: mRNA
 A.Residues: 1-24, 46-512 <STA>
 A.Cross-references: GB:M64608
 R.Yi, T.; Bolen, J.B.; Inle, J.N.
 Mol. Cell. Biol. 11, 2391-2398, 1991
 A>Title: Hematopoietic cells express two forms of lyn kinase differing by 21 amino acids
 A.Reference number: A39750; MUID:91203857; PMID:2017160
 A.Accession: A39750
 A.Molecule type: mRNA
 A.Residues: 1-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <YII>
 A.Cross-references: GB:M57696; NID:g198940; PIDN:AAA3471.1; PID:g198941
 A.Accession: B39750
 A.Molecule type: mRNA
 A.Residues: 1-24, 46-76, 'F', 78-160, 'I', 162-278, 'L', 280-390, 'I', 392-424, 'D', 426-512 <YII>
 A.Cross-references: GB:M57697; NID:g198942; PIDN:AAA3472.1; PID:g198943
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3
 C:Keywords: alternative splicing; ATP; autophosphorylation; blocked amino end; lipoprotein
 F1-512/Product: protein-tyrosine kinase lyn, long splice form #status predicted <MATL>
 F1-24, 46-512/Product: protein-tyrosine kinase lyn, short splice form #status predicted
 F170-118/Domain: SH3 homology <SH3>
 F129-226/Domain: SH2 homology <SH2>
 F245-504/Domain: protein kinase homology <KIN>
 F253-261/Region: protein kinase ATP-binding motif
 F12/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F275/Active site: lys #status predicted
 F397/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 27.5%; Score 371.5; DB 1; Length 512;
 Best Local Similarity 40.8%; Pred. No. 7, 4e-23;
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;

Qy 6 SRRKSLPSPSSVQGGCPVWMEARSKATVALGSPGAPRLSLALGSPRLTVSDD 65
 Db 38 SNKQGRVPER-HLPGQRFGTQDPEQSDIVVALYPDGIDHPPDSFFKGGKMKVLEEH 96
 Qy 66 GDMWTVLSEVSGREYNIPSVYAKV-----SHQWLYEGLSEKAEELLLPGNPGAFILIR 121
 Db 97 GEMWKAKSLSKREGFIPSNYAKVNTLTETEMWFKQITRQDAERQLAPGSGAGAFILIR 156
 Qy 122 ESOTRRGYSYLSVRLSRPASWDRIRHYRIHCLDNGMUYISPRLLTFPSLQALVDHYSELAD 181
 Db 157 ESETLKGFSLSVRLDYPDMHGDIKIKIRSLDNGYIISPRITPFCISDMIKYQKQSD 216
 Qy 182 DICLLKEPCVLAQRAPLPGK 202
 Db 217 GLCRLEKACI-----SPYPOK 233

RESULT 5
 TVNHUC
 protein-tyrosine kinase (EC 2.7.1.112) hck - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
 C/Accession: A27811; A27812; J01149; C38268; S31103
 R:Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.; Die
 Mol. Cell. Biol. 7, 2267-2275, 1987
 A>Title: Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and
 A.Reference number: A27811; MUID:87257942; PMID:3496523
 A.Accession: A27811
 A.Molecule type: mRNA
 A.Residues: 1-505 <QUI>
 A.Cross-references: GB:M16591
 A>Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' translation
 R:Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M.

Mol. Cell. Biol. 7, 2267-2285, 1987
 A>Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed in cells of h
 A.Reference number: A27812; MUID:87257943; PMID:3453117
 A.Accession: A27812
 A.Molecule type: mRNA
 A.Residues: 1-505 <ZIR>
 A.Cross-references: GB:M16592; NID:g183913; PIDN:AAA2644.1; PID:g306833
 R:Riedel, D.; Scherhardt, K.; Ruebsamen-Waigmann, H.
 Gene 113, 275-280, 1992
 A>Title: The genomic locus of the human hemopoietic-specific cell protein tyrosine kinase
 A.Reference number: J01149; MUID:92241680; PMID:1572549
 A.Accession: J01149
 A.Molecule type: DNA
 A.Residues: 157-505 <HRA>
 A.Cross-references: EMBL:X59741
 R:Partanen, J.; Maekela, T.P.; Altalo, R.; Lehtvaesalho, H.; Altalo, K.
 Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
 A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.
 A.Reference number: A38268; MUID:91062389; PMID:2247464
 A.Accession: C38268
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 362-417 <PAR>
 C/Genes: GDB:HCK
 A.Cross-references: GDB:119303; OMIM:142370
 A/Map position: 20q11-20q12
 A.Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
 C/Function:
 A>Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH3
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pho
 F164-112/Domain: SH3 homology <SH3>
 F123-220/Domain: SH2 homology <SH2>
 F239-497/Domain: protein kinase homology <KIN>
 F247-255/Region: protein kinase ATP-binding motif
 F2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F3/Binding site: palmitate (Cys) (covalent) #status predicted
 F268/Active site: lys #status predicted
 F390/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 27.0%; Score 364.5; DB 1; Length 505;
 Best Local Similarity 42.2%; Pred. No. 2, 7e-22;
 Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

Qy 12 PPSLSVSSVQGGCPVWMEARSKATVALGSPGAPRLSLALGSPRLTVSDDGWTV 71
 Db 40 PGNSHNS--NTEGIREAGSEDIIVVALYDEAIHHEDLSFQKDDQWVLEESGEWXA 96
 Qy 72 LSEVSGREYNIPSVYAKV-----SHQWLYEGLSEKAEELLLPGNPGAFILIR 127
 Db 97 RSLATRKSGYIPSNYAKVDSLETEWFFKISKDAERQLAPGNMGLSMIRDSITIK 156
 Qy 128 GSYSLSVRLSRPASWDRIRHYRIHCLDNGMUYISPRLLTFPSLQALVDHYSELADICLL 187
 Db 157 GSYSLSVRLDYPDMHGDIKIKIRSLDNGYIISPRITPFCISDMIKYQKQSD 216
 Qy 188 KEPCV 192
 Db 217 SVPCM 221

RESULT 6
 J01321
 protein-tyrosine kinase (EC 2.7.1.112) hck - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C/Accession: J01321; S18974
 C/Accession: J01321; S18974
 R:Okano, Y.; Sugimoto, Y.; Fukuko, M.; Matsui, A.; Nagata, K.; Nozawa, Y.
 Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
 A>Title: Identification of rat cDNA encoding hck tyrosine kinase from megakaryocytes.
 A.Reference number: J01321; MUID:92109719; PMID:1764064

A:Accession: J01321
 A:Molecule type: mRNA
 A:Residues: 1-503 <OKA>
 A:Cross-references: GB:S74141; NID:g241436; P1DN:AMB20754.1; P1D:g241437
 A:Experimental source: megakaryocyte
 A:Rema, V.; Swaid, G.
 submitted to the EMBL Data Library, December 1991
 A:Reference number: S18974
 A:Accession: S18974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-50, 'V', 52-204, 'R', 206-305, 'T', 307-503 <REM>
 A:Cross-references: EMBL:X62345; NID:g57581; P1DN:CAA44218.1; P1D:g57582
 C:Genetics:
 A:Gene: hck
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C:Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming protein kinase
 F:62-110/Domain: SH3 homology <SH3>
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase ATP-binding motif
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 26.5%; Score 357.5; DB 1; Length 503;
 Best Local Similarity 37.6%; Pred. No. 16-21; Indels 31; Gaps 5;
 Matches 86; Conservative 36; Mismatches 76; Indels 31; Gaps 5;

Qy 1 MGSLSR--RKSLSPELSSVQGGPYTME-----AERSKAT-A-37
 Db 1 MCGVSRFLREGSKAKIEPNANQPGVYDPPTSPKLGPNINSILPGFVGSSEDTIV-60
 Qy 38 VALGSPAGGPAELSLRGEPLTIVSESGREYNIPSVHYAKV---SHG-93
 Db 61 VALDYEAHREDSPKQDQVWVEESGEWKAFLATKKEGYIPSNVYARVNSLETET-120
 Qy 94 WLVEGLSRKEKEELLIPGPGAFILRESQTRGYSYSLVSLSPASMRIRHYIHL-153
 Db 121 WPFKGISRKDAERHLAPGMGSPFMRDSSTTGYSYSVDFPDQHDVVKHYKIRTL-180
 Qy 154 DNGWLISPRILTPSLQALVDHYSELADICLLKEPCVLOHAGLPCK-202
 Db 181 DSGGFYISPRSTFSSLOELVYHKKKGKGLQKLSVPCV---SPKPK-225

RESULT 7
 137206
 protein-tyrosine kinase (EC 2.7.1.112) b1k - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 04-Mar-2000
 C:Accession: I37206; S51647
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase ATP-binding motif
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

A:Accession: I37206
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-505 <RES>
 A:Cross-references: EMBL:Z33998; NID:g601951; P1DN:CAA83965.1; P1D:g601952
 C:Genetics:
 A:Gene: GDB:B1K
 A:Cross-references: GDB:454114; OMIM:191305
 A:Map position: 8p23-8p22
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C:Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphotransferase; tyrosine kinase homology <SH2>
 F:124-320/Domain: SH2 homology <SH2>
 F:239-497/Domain: protein kinase homology <KIN>
 F:247-253/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:269/Active site: Lys #status predicted

Query Match 26.4%; Score 356.5; DB 2; Length 505;
 Best Local Similarity 44.2%; Pred. No. 1,2e-21;
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;

Qy 25 PYTMEERKATNALVSLSPAGGPAELSLRGEPLTIVSESGREYNIPSVHYAKV---SHG-93
 Db 51 PDEHLEBDKHFVVALVDYTHMNDRLQMLKEGLQVLKGTGMWLASLVYEGEVPS-110
 Qy 85 VHYAKV---HGMYLEGLSRKEEELLIPGPGAFILRESQTRGYSYSLVSLRPPA-140
 Db 111 NFVARVLSLEMERWPFRRSQGKEAERQLAPINKAGFLIRSETTKGAFSLSVK-DVTT-169
 Qy 141 SMDIRHYRHLCDLGMVYSPRLTPSLQALVDHYSELADICLLKEPCV-192
 Db 170 QGELLIKHYKRLCDGCGYISPRITPSSLQALVQHSKQDGLCQRLTLPV-221

RESULT 8
 137206
 protein-tyrosine kinase (EC 2.7.1.112) hck - mouse
 N:Alternate names: kinase-related transforming protein (bmk)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 28-Jan-2000
 C:Accession: A27282; A39973
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase ATP-binding motif
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

A:Accession: A27282
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-503 <KLB>
 A:Cross-references: GB:Y00487; NID:g51209; P1DN:CAA6544.1; P1D:g51210
 R:Holzman, D.A.; Cook, W.D.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 8325-8329, 1987
 A:Title: Isolation and sequence of a cDNA corresponding to a src-related gene expressed in NIH3T3 cells
 A:Reference number: A39973; MUID:88068587; PMID:3317404
 A:Accession: A39973
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-503 <HOL>
 A:Cross-references: GB:Y003023; NID:g192212; P1DN:AAA37305.1; P1D:g309118
 C:Genetics:
 A:Gene: hck
 C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
 C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
 F:62-110/Domain: SH3 homology <SH3>
 F:121-218/Domain: SH2 homology <SH2>
 F:237-495/Domain: protein kinase ATP-binding motif
 F:245-253/Region: protein kinase ATP-binding motif
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F:3/Binding site: palmitate (Cys) (covalent) #status predicted
 F:267/Active site: Lys #status predicted
 F:388/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 26.4%; Score 356; DB 1; Length 503;
 Best Local Similarity 41.5%; Pred. No. 1,4e-21;
 Matches 83; Conservative 33; Mismatches 72; Indels 12; Gaps 4;

Qy 11 LPSPSLSSVQGGPYTME-----AERSKAT-AVALGSPAGGPAELSLRGEPLTIVSESG-66
 Db 30 VPDPTSSKLGPNNSNMPGVEGSEDTIVVALDYEAHREDSPKQDQVWVEEG-89
 Qy 67 DWWTYLSVSGREYNIPSVHYAKV---SHGMYLEGLSRKEEELLIPGPGAFILRESQTRGYSYSLVSLRPPA-140
 Db 90 EWMKARSATLKKEGYIPSNVYARVNSLETETWPFKISRKDAERHLAPGMGSPFMRDSSTTGYSYSVDFPDQHDVVKHYKIRTL-180
 Qy 123 SQTRRGYSYSLVSLRPPASMDIRHYRHLCDLGMVYSPRLTPSLQALVDHYSELAD-182
 Db 150 SETTGYSYSLVSRDPDQHDVVKHYKIRTLDSGCGYISPRSTFSSLOELVYHKKKGKDG-209

Qy 189 ICCLKEPCVLQKAPGLPGK 202
Db 210 LQKLSVPCV-----SPKPK 225

RESULT 9

A40092
protein-tyrosine kinase (EC 2.7.1.112) blk [validated] - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C:Accession: A40092

R:Diyeck, S.M.; Niederhuber, J.E.; Desiderio, S.V.

Science 247, 332-336, 1990

A>Title: Specific expression of a tyrosine kinase gene, blk, in B lymphoid cells.

A:Reference number: A40092; MUID:90117147; PMID:2404338

A:Accession: A40092

A:Molecule type: mRNA

A:Residues: 1-499 <DYM>

A:CROSS-references: GB:M0903; NID:g202076; PIDN:AAA0453.1; PID:g202077

C:Genetics:

A:Gene: MGI:Blk

A:CROSS-references: MGI:88169

A:Map position: 14:28.0

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc

F:118-214/Domain: SH2 homology <SH2>

F:243-491/Domain: protein kinase homology <KIN>

F:241-249/Region: protein kinase ATP-binding motif

F:263/Active site: myristylated amino end (Gly) (in mature form) #status predicted

Query Match 25.8%; Score 348.5; DB 1; Length 499;

Best Local Similarity 36.5%; Pred. No. 5.66-21;

Matches 81; Conservative 32; Mismatches 72; Indels 37; Gaps 4;

Qy 1 MGSLPSRKSLSPLSSVGGQPV-----TMEERSK 34

Db 1 MGLSSRQ-----VSEKKGKSPVKIRTDKAPPLPLVFNHLPSPNDPDEE 54

Qy 35 ATAVALGSPFAGPAELSLRGEPLTVSESDGDMWTVLSEVSEVNVAVKVS--- 91

Db 55 RFVVALFDVAANVDLDVLRGELQVLRSTGDMWLASLVTEGEGVSNVAVETLE 114

Qy 92 -HGMVLEGLSRKAEELLILPFGNCGAFILRSQTRRSYSLSRLSPASMDRIHYRI 150

Db 115 VKKFFFTISRKDAERQLLAPMNAKGFILRSSESNKGAFLSVK-DITTOGEVYKHYKI 173

Qy 151 HCLDNGMLYISPLTFPSLQALVDHSELAADDICCLKEPCV 192

Db 174 RSLDNGGYISPLTFPSLQALVDHSELAADDICCLKEPCV 215

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

Qy 10

Db 10

A:Molecule type: mRNA

A:Residues: 1-86; 'P', 88-509 <PER>

A:CROSS-references: EMBL:X13529; NID:g34294; PIDN:CAA31884.1; PID:g34295

R:Koga, Y.; Caccia, N.; Toyonaga, B.; Spolski, R.; Yanagi, Y.; Yoshikai, Y.; Mak, T.W.

Eur. J. Immunol. 16, 1643-1646, 1986

A>Title: A human T cell-specific cDNA clone (Y116) encodes a protein with extensive hom

A:Reference number: S07200; MUID:8733831; PMID:3493153

A:Accession: S07200

A:Molecule type: mRNA

A:Residues: 1-205; 'ASAIPY', 212-257, 'KCGW', 262, 'TTT', 266, 'T', 268-281, 'AGRLP', 287-503, 'ST

A:CROSS-references: EMBL:X05021; NID:g36807; PIDN:CAA28691.1; PID:g36808

R:Veilleux, A.; Foss, F.M.; Sauvillie, E.A.; Bolen, J.B.; Rosen, N.

Oncogene Res. 1, 357-374, 1987

A>Title: Expression of the lck tyrosine kinase gene in human colon carcinoma and other r

A:Reference number: S01879; MUID:88217332; PMID:2835736

A:Accession: S01879

A:Molecule type: mRNA

A:Residues: 368-471, 'H', 473-509 <VEI>

A:CROSS-references: EMBL:X06369; NID:g34288; PIDN:CAA29667.1; PID:g34289

R:Trevillian, J.M.; Lin, Y.; Chen, S.J.; Phillips, C.A.; Canna, C.; Lina, T.J.

Biochim. Biophys. Acta 888, 286-295, 1986

A>Title: Human T lymphocytes express a protein-tyrosine kinase homologous to p56 (LSTRA)

A:Reference number: S07143; MUID:87000726; PMID:3489486

A:Accession: S07143

A:Molecule type: mRNA

A:Residues: 'A', 378-509 <TRB>

A:CROSS-references: EMBL:X04476; NID:g35779; PIDN:CAA28165.1; PID:g35780

R:Takadera, T.; Leung, S.; Gernone, A.; Koga, Y.; Takihara, Y.; Miyamoto, N.G.; Mak, T.W.

Mol. Cell. Biol. 9, 2173-2180, 1989

A>Title: Structure of the two promoters of the human lck gene: differential accumulation

A:Reference number: A22797; MUID:89313764; PMID:2787474

A:Accession: A32797

A:Molecule type: DNA

A:Residues: 1-35 <TRK>

A:CROSS-references: GB:M26692; NID:g341533; PIDN:AAA59503.1; PID:g349702

R:Garvin, A.M.; Pawar, S.; March, J.D.; Perlmuter, R.M.

Mol. Cell. Biol. 8, 3058-3064, 1988

A>Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell

A:Reference number: 157636; MUID:89096991; PMID:2850479

A:Accession: 157636

A:Molecule type: DNA

A:Residues: 1-35, 'VR', <RES>

A:CROSS-references: GB:M21510; NID:g187031; PIDN:AAA59501.1; PID:g553522

C:Comment: Protein tyrosine kinases play important roles in the control of cell growth a

C:Genetics:

A:Gene: GDB:LCK

A:CROSS-references: GDB:119360; OMIM:153390

A:Map position: 1p35-1p34.3

A:Insertions: 35/3; 63/1; 93/2; 126/2; 161/1; 262/1; 322/1; 347/3; 399/1; 443/1

C:Function:

A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP

C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pnc

F:2-509/Product: protein-tyrosine kinase lck #status predicted <MNI>

F:68-116/Domain: SH3 homology <SH3>

F:127-224/Domain: SH2 homology <SH2>

F:243-501/Domain: protein kinase homology <KIN>

F:251-259/Region: protein kinase ATP-binding motif

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3.5/Binding site: palmitate (Cys) (covalent) #status predicted

F:273/Active site: Lys #status predicted

F:394,505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match

Best Local Similarity 25.5%; Score 344; DB 1; Length 509;

Matches 74; Conservative 26; Mismatches 70; Indels 10; Gaps 2;

Qy 26 VTMEERSKAT-----AVAGSPFAGPAELSLRGEPLTVSESDGDMWTVLSEVSGRE 79

Db 49 VTVEGSPFAGPAELSLRGEPLTVSESDGDMWTVLSEVSGRE 108

Qy 80 YNIPSVHAKVS-----HGMVLEGLSRKAEELLILPFGNCGAFILRSQTRRSYSLSRLSPASMDRIHYRI 135

DB 109 GTFPNTYAKANSLPEPEPFKNSLRDARQLALAGNTHGSFILRESESTAGSSLSLR 166
 QY 136 LSRPASMDRIRRHRIHCLDNGMLYISPLTPSPQLADYHSELAADICCLKEPCVQR 195
 DB 169 DFQDQGVVYKHYKIRNLNDGFGYISPRITPGIHLVYHYNASDGLCTRLSRPCQTOK 228

RESULT 11

148845
 protein-tyrosine kinase (EC 2.7.1.112) lck, lymphocyte - mouse

N/Alternate names: p56; protein-tyrosine kinase lck

C/Species: Mus musculus (house mouse)

C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 03-Mar-2000

C/Accession: 148845; A23639; I57629; I77452

R/Voronova, A.F.; Sefton, B.M.

A/Title: Expression of a new tyrosine protein kinase is stimulated by retrovirus promote

A/Reference number: 148845; PMID:86146842; PMID:3081813

A/Accession: 148845

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-509 <VOR1>

A/Cross-references: EMBL:X03533; NID:954813; PIDN:CAA27234.1; PID:954814

R/Marth, J.D.; Peet, R.; Krebs, E.G.; Perlmutter, R.M.

A/Title: A lymphocyte-specific protein-tyrosine kinase gene is rearranged and overexpress

A/Reference number: A23639; PMID:86079521; PMID:2416464

A/Accession: A23639

A/Molecule type: mRNA

A/Residues: 1-282; 'VR', 285-509 <MAR>

A/Cross-references: GB:M12056; NID:9198763

A/Note: the sequence is revised in Genbank entry MUSLCK, release 116.0, (PIDN:AA59674.1

R/Voronova, A.F.; Adler, H.T.; Sefton, B.M.

Mol. Cell. Biol. 7, 4407-4413, 1987

A/Title: Two lck transcripts containing different 5' untranslated regions are present in

A/Reference number: I57629; PMID:86142832; PMID:3501824

A/Accession: I57629

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-11 <VOR>

A/Cross-references: GB:M18098; NID:9198766; PIDN:AAA39422.1; PID:9198767

R/Garvin, A.M.; Pawar, S.; Marth, J.D.; Perlmutter, R.M.

Mol. Cell. Biol. 8, 3058-3064, 1988

A/Title: Structure of the murine lck gene and its rearrangement in a murine lymphoma cell

A/Reference number: I57636; PMID:89096891; PMID:2850479

A/Accession: I77452

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-35, 'VR', <GAR>

A/Cross-references: GB:M21511; NID:9198768; PIDN:AAA39422.1; PID:9554186

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C/Keywords: ATP; autophosphorylation; blocked amino end; kinase-related transforming pro

F/68-116/Domain: SH3 homology <SH3>

F/127-224/Domain: SH2 homology <SH2>

F/243-501/Domain: protein kinase homology <KIN>

F/251-259/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/273/Active site: Lys #status predicted

F/394/505/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match 25.4%; Score 342.5; DB 1; Length 509;

Best Local Similarity 39.6%; Pred. No. 1.8e-20;

Matches 78; Conservative 28; Mismatches 84; Indels 7; Gaps 2;

QY 3 SLPSRRKSLPSPLSSVQGGVPTWEARSKATAVALGSPGAPAEISRLGEPPLTV 62
 DB 35 SLPIRNGSEVRDPL---VTYEGSLPASPDLQNLVIALHVSERSHGDGFEKGEQRL 91
 QY 63 SEDGDWWTYLSVSGREINIPSVYAKV---HGMVEGSEKSEKELLIPNPGCAP 118
 DB 92 EQSGEWMKAKQSLTGGEGFIPFNFAKANSLPEPEPFKNSLRDARQLALAGNTHGS 151

QY 119 LIREQTRGSGYSLSVRLSRPASMDRIRRHRIHCLDNGMLYISPRITPGIADYHYSK 178
 DB 152 LIRESESTAGSSLSVRDQDQGVVYKHYKIRNLNDGFGYISPRITPGIHLVYHYN 211
 QY 179 LADICCLKEPCVQR 195
 DB 212 ASBGLCTRLSRPCQTOK 228

RESULT 12

A39939
 protein-tyrosine kinase (EC 2.7.1.112) ckl [similarity] - chicken

N/Alternate names: kinase-related transforming protein (tkl); T-cell surface antigen aas

C/Species: Gallus gallus (chicken)

C/Date: 16-Jun-2000 #sequence_revision 16-Jun-2000 #text_change 16-Jun-2000

C/Accession: A42126; A39939

R/Chow, L.M.; Ratcliffe, M.J.; Veilleux, A.

Mol. Cell. Biol. 12, 1226-1233, 1992

A/Title: ckl is the avian homolog of the mammalian lck tyrosine protein kinase gene.

A/Reference number: A42126; PMID:92186854; PMID:1545804

A/Accession: A42126

A/Molecule type: mRNA

A/Residues: 1-88 <CHO>

A/Cross-references: GB:M85043

A/Experimental source: thymus, spleen

A/Note: sequence extracted from NCBI backbone (NCBIN:88831, NCBI:88833)

R/Strebhardt, K.; Mullins, J.I.; Bruck, C.; Ruebsamen-Waigmann, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 8778-8782, 1987

A/Title: Additional member of the protein-tyrosine kinase family: the src-and lck-relat

A/Reference number: A39939; PMID:86097370; PMID:3321053

A/Accession: A39939

A/Molecule type: mRNA

A/Residues: 52-507 <STR>

A/Cross-references: GB:J03579; NID:9212712; PIDN:AAA9081.1; PID:9212713

C/Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h

C/Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; ph

F/66-114/Domain: SH3 homology <SH3>

F/125-222/Domain: SH2 homology <SH2>

F/241-499/Domain: protein kinase homology <KIN>

F/249-257/Region: protein kinase ATP-binding motif

F/2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F/392/503/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pre

Query Match

Best Local Similarity 24.9%; Score 337; DB 1; Length 507;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

QY 38 VALGSPAGAPAEISRLGEPPLTVSDDGPMWTVLSVSGREYVIPSVYAKV---HG 93
 DB 65 VALDYEPETHDGLGKQEKLRVBSGEMWKAQSLTGGEGILPNNFYAMNLSLEPEP 124

QY 94 WLTEGLREKAEELLPLPNPGAFILRESQTRGSGYSLSVRLSRPASMDRIRRHRIHCL 153
 DB 125 WPKNLKSKNAEARLLASGNTGSLIRESETSKGSYSLSVDPDQNGRTVYKIRNM 184

QY 154 DNGMLYISPRITPGIADYHYSLEADDDICCLKEPCVQR 195
 DB 185 DNGGYISPRVTSIHLBEVYSSSDGLCTRLGKPCQTOK 226

RESULT 13

B49114
 protein-tyrosine kinase (EC 2.7.1.112) ftk - Pacific electric ray

C/Species: Torpedo californica (Pacific electric ray)

C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 18-Feb-2000

C/Accession: B49114

R/Swope, S.L.; Huganir, R.L.

J. Biol. Chem. 268, 25152-25161, 1993

A/Title: Molecular cloning of two abundant protein tyrosine kinases in Torpedo electric

A/Reference number: A49114; PMID:9404336; PMID:8227079

A/Accession: B49114

A/Status: preliminary

A/Molecule type: mRNA

A:Residues: 1-539 <SMO>
A:Cross-references: GB:U01350
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology; SH3 p
C:Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; phospho
F:91-140/Domain: SH2 homology <SH2>
F:151-248/Domain: SH2 homology <SH2>
F:271-529/Domain: protein kinase homology <KIN>
F:279-287/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:301/Active site: Lys #status predicted
F:422,533/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	24.4%	Score 329;	DB 2;	Length 539;
Best Local Similarity	41.5%;	Pred. No. 2.5e-19;		
Matches	76;	Conservative	27;	Mismatches 66;
				Indels 14;
				Gaps 4;

```

QY 15 SLSSVQOC-OCPYVMEARESKATAAAGSPAGPAEALSLRGEPLTV-SDSGMWIVL 72
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 74 SLTSRGVGTGCVTM-----FTALYNDATEDDLPFKGSEKPHIINSSGDMWEAR 125
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 73 SEVSGREYNIPSVYAKV---SHGMLEYGLSREKAEILLPLPNPGCAF.LRESQTRG 128
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 126 SLTTSSTGYISNNYVA.PVDSIAEWEFGMGKKDTERMLLCPNPGFTPLIRESETTKG 165
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 129 SYSLSVLRSLRSPASHDRIRRYIRHCLDNGMLYISPRLTPEPSIALVDHYSELADICLLK 188
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 186 AYSLSIRPMDEWKGVDKWKYKIRKLDNGYIITTRAQFETVPQLVHHYTERBAAGCRLV 245
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 189 EPC 191
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 246 VPC 248

```

RESULT 14

TVFVG9

protein-tyrosine kinase (EC 2.7.1.112) yes - avian sarcoma virus Y73
C:Species: avian sarcoma virus Y73
A:Note: host Gallus gallus (chicken)
C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #ext_change 23-Feb-1997
C:Accession: A00633
R:Kitamura, N.; Kitamura, A.; Toyoshima, K.; Hirayama, Y.; Yoshida, M.
Nature 297, 205-208, 1982
A:Title: Avian sarcoma virus Y73 genome sequence and structural similarity of its trans-
A:Reference number: A00633; WUID:82195528; PMID:6281656
A:Accession: A00633
A:Molecule type: genomic RNA
A:Residues: 1-528 <KIT>
C:Comment: This protein is synthesized as a gag-yes polyprotein.
C:Gene(s):
A:Gene(s): yes
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 homology
C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; trans-
F:88-117/Domain: SH3 homology <SH3>
F:148-245/Domain: SH2 homology <SH2>
F:265-523/Domain: protein kinase homology <KIN>
F:273-281/Region: protein kinase ATP-binding motif
F:295/Active site: Lys #status Predicted
F:416/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status Predicted

Query Match	24.08;	Score 324;	DB 1;	Length 528;
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Qy      2  GSLPRRRKSLPSLSLSSVOGGPVTMEARSRATATVALTSFPAGCAPSLRLGPELTI 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62  GGASSSPSNPSP-YSTILTGGTV-----FALVDYEAKRTDLSFKKERNPQI 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      62  VSE-DGDMWTVLSEVSGREYIPSVYHAKY---SHGLVYGLSRKAEELLILPGNPG 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      111  INMTEGGMEARSIATGKTGYPSNYVAADSLQAEEMVPEFGKGRDARLLINPNQNRG 170
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy      117  AFLRESQGTARGSYSLVRLSRPASNRI-----HYHICLDNGMLYISPLTFPSLQA 171
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 171 IFLVSEETTKGAALSTIR-----DMDEVGVDVHKYIRLNDGNGYITTPAGEBLSJK 225
Qy 172 LVDRHSELADIDICLLKERC-----VLQAGPLRGKDIPLUPTVQR----- 212
Db 226 LVNHRREHBDLCHKLTTCFVPCVQPGQIAKAMEIRBSIRLVLTAGCGCFGEVMNGT 285
Qy 213 -----TPLMKELDSLLSBEAATGBESLLSEGLRSL-SPTISLNDPAV 256
Db 286 MNGTITKVAIKTLKGTGMBEALDEADQIMKRLHNDLVLPLVAAYVEEPI 334

```

RESULT 15

protein-tyrosine kinase (EC 2.7.1.112) yes [similarity] - African clawed frog
N/Alternate names: kinase-related transforming protein (yes)

C:Date: 16-Jun-2000
C:Defect: amino acid sequence
C:Release: 16-Jun-2000
C:Accession: A45501; S08517
R:Steele, R.E.; Iwlin, M.Y.; Knudsen, C.L.; Collect, J.W.; Fero, J.B.
Oncogene Res. 1, 223-233, 1989
A:Title: The yae proto-oncogene is present in amphibians and contributes to the maternal
A:Reference number: A45501
A:Accession number: A45501
A:Molecule type: mRNA
A:Residues: 1-537 <STB>
A:Cross-references: GB:X14377
R:Steele, R.E.; Iwlin, M.Y.; Knudsen, C.L.; Collect, J.W.; Fero, J.B.
submitted to the EMBL Data Library, February 1989
A:Reference number: S08517
A:Accession number: S08517
A:Molecule type: mRNA
A:Residues: 1-250, 'S', 252-537 <STB>
A:Cross-references: EMBL:X14377; NID:G65272; PIDN:CAA32551.1; PID:G65273
C:Genetics:
A:Gene: yae8
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3 h
A:Keywords: ATP, autophosphorylation; blocked amino end; kinase-related transforming pro
F:92-141/Domain: SH3 homology <SH3>
F:152-249/Domain: SH2 homology <SH2>
F:269-527/Domain: protein kinase homology <KIN>
F:277-285/Region: protein kinase ATP-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:229/Active site: lys #status predicted
F:450_531/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status pred

Query Match	23.9%;	Score 323.5;	DB 1;	Length 537;
Best Local Similarity	33.6%;	Pred. No. 7.1e-19;		
Matches	85;	Conservative	38;	Mismatches 91;
				Indels 39;
				Gaps 7;

QY 38 VALGFFAGCPALSLIRGEPLTVSE -GDDMMTVLSEVSGREXNIPSYHVAKV-----SH 92

Db 91 VALVYEAFRTTELSRKGEEFFQIINNTGDDWMEARSJATGKTGYIPSNVYVAPADSIQAE 150

QY 93 GMLYEGLSREKABELLLPGAPGAPFLIRESGTREGSYSLVLSHRPASWBIR-----H 147

Db 151 EMYGFGKGRDARILLNPGNRGTFLVRESSTTGAISLSIR-----DMBEYGDQNVKH 205

QY 148 YAHNGLNGLYISPLTFPFLQALVDHSELAADIICLLKEPC-----VLQDAGR 198

Db 206 YKIRLNDNGYITTTTRAQEBSLQLYAHVSEHADDCLRLTLVCPYVKRQTQGLAKDAMW 265

QY 199 LPQKIDPLPYTVTOR-----TPLNKKELDSSLFSEATGSEBSLSEGLRES 244

Db 266 IIRSELRLDVLQGGQGFSEWITGMNGTKTKVALIKTLKGTMMPEARLQEAQIMKKLNDHK 325

QY 245 L-SFYISLNDKAV 256

Db 326 LVPLVAVVSEEP 338

Search completed: March 24, 2003, 15:51:36
Job time : 25.1455 secs

